==========

Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=3; day=20; hr=17; min=21; sec=17; ms=821;]

==========

****

Reviewer Comments:

<400> 696

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      Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                   20                  25                  30
      Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
               35                  40                  45
      Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
           50                  55                  60
      His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
       65                  70                  75                  80
      Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Xaa
                       85                  90                  95
      Gly Lys Glu Tyr Lys Cys Lys Val Ser Xaa Lys Gly Leu Pro Ser Ser
                  100                 105                 110
      Ile Glu Lys Thr Ile Ser Xaa Ala Xaa Gly Gln Pro Arg Glu Pro Gln
              115                 120                 125
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Per the above sequence id# 696, please explain "Xaa" at locations 96, 106, 119 and 121. Please check the remaining sequences for similar errors.

****

Validated By CRFValidator v 1.0.3

Application No: 10566409 Version No: 1.0

Input Set:

Output Set:

Started: 2009-02-26 18:37:15.342
Finished: 2009-02-26 18:37:59.763
Elapsed: 0 hr(s) 0 min(s) 44 sec(s) 421 ms
Total Warnings: 631
Total Errors: 13
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)
W	213	Artificial or Unknown found in <213> in SEQ ID (27)
W	213	Artificial or Unknown found in <213> in SEQ ID (28)
W	213	Artificial or Unknown found in <213> in SEQ ID (29)
W	213	Artificial or Unknown found in <213> in SEQ ID (30)
W	213	Artificial or Unknown found in <213> in SEQ ID (31)
W	213	Artificial or Unknown found in <213> in SEQ ID (32)
W	213	Artificial or Unknown found in <213> in SEQ ID (33)
W	213	Artificial or Unknown found in <213> in SEQ ID (34)
W	213	Artificial or Unknown found in <213> in SEQ ID (35)
W	213	Artificial or Unknown found in <213> in SEQ ID (36)
W	213	Artificial or Unknown found in <213> in SEQ ID (37)
W	213	Artificial or Unknown found in <213> in SEQ ID (38)
W	213	Artificial or Unknown found in <213> in SEQ ID (39)
W	213	Artificial or Unknown found in <213> in SEQ ID (40)
W	213	Artificial or Unknown found in <213> in SEQ ID (41)
W	213	Artificial or Unknown found in <213> in SEQ ID (42)
W	213	Artificial or Unknown found in <213> in SEQ ID (43)
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Input Set:

Output Set:

Started: 2009-02-26 18:37:15.342
Finished: 2009-02-26 18:37:59.763
Elapsed: 0 hr(s) 0 min(s) 44 sec(s) 421 ms
Total Warnings: 631
Total Errors: 13
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code		Error Description
		This error has occured more than 20 times, will not be displayed
W	402	Undefined organism found in <213> in SEQ ID (201)
W	402	Undefined organism found in <213> in SEQ ID (202)
W	402	Undefined organism found in <213> in SEQ ID (203)
W	402	Undefined organism found in <213> in SEQ ID (204)
W	402	Undefined organism found in <213> in SEQ ID (205)
W	402	Undefined organism found in <213> in SEQ ID (206)
E	257	Invalid sequence data feature in <221> in SEQ ID (212)
E	257	Invalid sequence data feature in <221> in SEQ ID (216)
W	402	Undefined organism found in <213> in SEQ ID (451)
W	402	Undefined organism found in <213> in SEQ ID (452)
W	402	Undefined organism found in <213> in SEQ ID (457)
W	402	Undefined organism found in <213> in SEQ ID (458)
W	251	Found intentionally skipped sequence in SEQID (520)
W	251	Found intentionally skipped sequence in SEQID (521)
W	251	Found intentionally skipped sequence in SEQID (522)
W	251	Found intentionally skipped sequence in SEQID (523)
W	251	Found intentionally skipped sequence in SEQID (524)
W	251	Found intentionally skipped sequence in SEQID (525)
W	251	Found intentionally skipped sequence in SEQID (526)
W	251	Found intentionally skipped sequence in SEQID (527)
W	251	Found intentionally skipped sequence in SEQID (639)

Input Set:

Output Set:

Started: 2009-02-26 18:37:15.342
Finished: 2009-02-26 18:37:59.763
Elapsed: 0 hr(s) 0 min(s) 44 sec(s) 421 ms
Total Warnings: 631
Total Errors: 13
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code		Error Description
W	251	Found intentionally skipped sequence in SEQID (640)
W	251	Found intentionally skipped sequence in SEQID (643)
W	251	Found intentionally skipped sequence in SEQID (646)
W	251	Found intentionally skipped sequence in SEQID (680)
W	251	Found intentionally skipped sequence in SEQID (681)
E	257	Invalid sequence data feature in <221> in SEQ ID (685)
E	257	Invalid sequence data feature in <221> in SEQ ID (685)
E	257	Invalid sequence data feature in <221> in SEQ ID (685)
W	251	Found intentionally skipped sequence in SEQID (688)
W	251	Found intentionally skipped sequence in SEQID (689)
E	257	Invalid sequence data feature in <221> in SEQ ID (696)
E	257	Invalid sequence data feature in <221> in SEQ ID (696)
E	257	Invalid sequence data feature in <221> in SEQ ID (696)
E	257	Invalid sequence data feature in <221> in SEQ ID (696)
E	341	'Xaa' position not defined SEQID (696) POS (96)
E	341	'Xaa' position not defined SEQID (696) POS (106)
E	341	'Xaa' position not defined SEQID (696) POS (119)
E	341	'Xaa' position not defined SEQID (696) POS (121)
W	251	Found intentionally skipped sequence in SEQID (699)

<110> Ledbetter, Jeffrey A.
Hayden-Ledbetter, Martha S.
Thompson, Peter A.

<120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.40102USPC

<140> 10566409
<141> 2009-02-26

<150> PCT/US2003/041600
<151> 2003-12-24

<150> US 10/627,556
<151> 2003-07-26

<150> US 10/053,530
<151> 2002-01-17

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<213> Homo sapiens
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atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 180
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 240
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 300
tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 360
gagaaaacaa tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 420
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 480
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 540
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 600
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 660
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatgatc taga 714

<210> 2
<211> 235
<212> PRT
<213> Homo sapiens
<400> 2
Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
1 5 10 15
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
20 25 30
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
35 40 45

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
50 55 60
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65 70 75 80
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
85 90 95
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
100 105 110
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
115 120 125
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
130 135 140
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145 150 155 160
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
165 170 175
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
180 185 190
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
195 200 205
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
210 215 220
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235

<210> 3
<211> 718
<212> DNA
<213> Lama glama
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<221> modified_base
<222> (34)..(34)
<223> n is a, c, g, or t
<220>
<221> modified_base
<222> (43)..(43)
<223> n is a, c, g, or t
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<222> (52)..(52)
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<222> (55)..(55)
<223> n is a, c, g, or t
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<222> (58)..(58)
<223> n is a, c, g, or t
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<222> (64)..(64)
<223> n is a, c, g, or t
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actnccagga ggcccttctg tctttgtctt ccccccgaaa cccaaggacg tcctctccat 120
ttttggaggc cgagtcacgt gcgttgtagt ggacgtcgga aagaaagacc ccgaggtcaa 180

tttcaactgg tatattgatg gcgttgaggt gcgaacggcc aatacgaagc caaaagagga 240
acagttcaac agcacgtacc gcgtggtcag cgtcctgccc atccagcacc aggactggct 300
gacggggaag gaattcaagt gcaaggtcaa caacaaagct ctcccggccc ccatcgagag 360
gaccatctcc aaggccaaag ggcagacccg ggagccgcag gtgtacaccc tggccccaca 420
ccgggaagaa ctggccaagg acaccgtgag cgtaacatgc ctggtcaaag gcttctaccc 480
agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc 540
caacacgccg ccacagctgg acaacgacgg gacctacttc ctctacagca agctctcggt 600
gggaaagaac acgtggcagc ggggagaaac cttaacctgt gtggtgatgc atgaggccct 660
gcacaaccac tacacccaga aatccatcac ccagtcttcg ggtaaatagt aatctaga 718

<210> 4
<211> 231
<212> PRT
<213> Lama glama
<400> 4

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Glu Pro His Gly Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu
1               5                  10                  15
Pro Gly Gly Pro Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val
            20                  25                  30
Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45
Gly Lys Glu Asp Pro Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val
    50                  55                  60
Glu Val Arg Thr Ala Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
65                  70                  75                  80
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
                85                  90                  95
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
            100                 105                 110
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
        115                 120                 125
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
    130                 135                 140
Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn
145                 150                 155                 160
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
                165                 170                 175
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
            180                 185                 190
Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr
        195                 200                 205
Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220
Ile Thr Gln Ser Ser Gly Lys
225                 230
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<210> 5
<211> 757
<212> DNA
<213> Lama glama
<400> 5

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catcttcccc ccgaaaccca aggacgtcct ctccatttct gggaggcccg aggtcacgtg 180
cgttgtggta gacgtgggcc aggaagaccc cgaggtcagt ttcaactggt acattgatgg 240
cgctgaggtg cgaacggcca acacgaggcc aaaagaggaa cagttcaaca gcacgtaccg 300
cgtggtcagc gtcctgccca tccagcacca ggactggctg acggggaagg aattcaagtg 360

caaggtcaac aacaaagctc tcccggcccc catcgagaag accatctcca aggccaaagg 420
gcagacccgg gagccgcagg tgtacaccct ggccccacac cgggaagagc tggccaagga 480
caccgtgagc gtaacatgcc tggtcaaagg cttctaccca cctgatatca acgttgagtg 540
gcagaggaat gggcagccgg agtcagaggg cacytacgcc accacgccac cccagctgga 600
caacgacggg acctacttcc tctacagcaa gctctcggtg ggaaagaaca cgtggcagca 660
gggagaaacc ttcacctgtg tggtgatgca cgaggccctg cacaaccact acacccagaa 720
atccatcacc cagtcttcgg gtaaatagta atctaga 757

<210> 6
<211> 248
<212> PRT
<213> Lama glama
<400> 6

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Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln
1               5                  10                  15
Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu
            20                  25                  30
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
        35                  40                  45
Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp
    50                  55                  60
Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly
65                  70                  75                  80
Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn
                85                  90                  95
Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
            100                 105                 110
Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro
        115                 120                 125
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
    130                 135                 140
Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp
145                 150                 155                 160
Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile
                165                 170                 175
Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr
            180                 185                 190
Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr
        195                 200                 205
Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe
    210                 215                 220
Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
225                 230                 235                 240
Ser Ile Thr Gln Ser Ser Gly Lys
                245
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<210> 7
<211> 727
<212> DNA
<213> Lama glama
<400> 7

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actccttgga gggcccacgg tcttcatctt ccccccgaaa gccaaggacg tcctctccat 120
cacccgaaaa cctgaggtca cgtgcttgtg gtggacgtgg gtaaagaaga ccctgagatc 180
gagttcaagc tggtccgtgg atgacacaga ggtacacacg gctgagacaa agccaaagga 240
ggaacagttc aacagcacgt accgcgtggt cagcgtcctg cccatccagc accaggactg 300
gctgacgggg aaggaattca agtgcaaggt caacaacaaa gctctcccag cccccatcga 360

gaggaccatc tccaaggcca aagggcagac ccgggagccg caggtgtaca ccctggcccc 420
acaccgggaa gagctggcca aggacaccgt gagcgtaacc tgcctggtca aaggcttctt 480
cccagctgac atcaacgttg agtggcagag gaatgggcag ccggagtcag agggcaccta 540
cgccaacacg ccgccacagc tggacaacga cgggacctac ttcctctaca gcaaactctc 600
cgtgggaaag aacacgtggc agcagggaga agtcttcacc tgtgtggtga tgcacgaggc 660
tctacacaat cactccaccc agaaatccat cacccagtct tcgggtaaat agtaatctag 720
agggccc 727

<210> 8
<211> 236
<212> PRT
<213> Lama glama
<400> 8

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1				5				10					15		
Pro	Gly	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Thr	Val	Phe	Ile	Phe	Pro	Pro
			20					25					30		
Lys	Ala	Lys	Asp	Val	Leu	Ser	Ile	Thr	Arg	Lys	Pro	Glu	Val	Thr	Cys
		35					40					45			
Leu	Trp	Trp	Thr	Trp	Val	Lys	Lys	Thr	Leu	Arg	Ser	Ser	Ser	Ser	Trp
	50					55					60				
Ser	Val	Asp	Asp	Thr	Glu	Val	His	Thr	Ala	Glu	Thr	Lys	Pro	Lys	Glu
65					70					75					80
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln
				85					90					95	
His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn
			100					105					110		
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly
		115					120					125			
Gln	Thr	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu
	130					135					140				
Leu	Ala	Lys	Asp	Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Phe
145					150					155					160
Pro	Ala	Asp	Ile	Asn	Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser
				165					170					175	
Glu	Gly	Thr	Tyr	Ala	Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr
			180					185					190		
Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Gln
		195					200					205			
Gly	Glu	Val	Phe	Thr	Cys	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His
	210					215					220				
Ser	Thr	Gln	Lys	Ser	Ile	Thr	Gln	Ser	Ser	Gly	Lys				
225					230					235					

<210> 9
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<212> DNA
<213> Homo sapiens
<400> 9
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<210> 10
<211> 18
<212> PRT
<213> Homo sapiens
<400> 10

Asp	Gln	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys

1 5 10 15
Pro Ala

<210> 11
<211> 54
<212> DNA
<213> Homo sapiens
<400> 11
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<210> 12
<211> 18
<212> PRT
<213> Homo sapiens
<400> 12
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1 5 10 15
Pro Ala

<210> 13
<211> 327
<212> DNA
<213> Homo sapiens
<400> 13
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atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 120
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 180
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 300
atcgagaaaa ccatctccaa agccaaa 327

<210> 14
<211> 109
<212> PRT
<213> Homo sapiens
<400> 14
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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
35 40 45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65 70 75 80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
85 90 95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 15
<211> 324
<212> DNA
<213> Homo sapiens
<400> 15
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 180
gacggctcct tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300
ctctccctgt ccccgggtaa atga 324

<210> 16
<211> 107
<212> PRT
<213> Homo sapiens
<400> 16

Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu
1				5				10					15		
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
		20					25					30			
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	35					40					45				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
50					55					60					
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
65				70					75					80	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
			85					90					95		
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
		100					105								

<210> 17
<211> 54
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gatcaggagc ccaaatcttc tgacaaaact cacacatccc caccgtcccc agca 54

<210> 18
<211> 18
<212> PRT
<213> Homo sapiens
<400> 18

Asp	Gln	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser
1				5				10					15		
Pro	Ala														

<210> 19
<211> 712
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Synthetic
nucleotide sequence
<400> 19
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